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(FILE 'HOME' ENTERED AT 15:06:08 ON 30 SEP 2003)
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L1 9161 S MASS SPECTRO? AND (GEL OR ELECTROPHOR?)
L2 1459 S LASER(2A)(DESOR? OR ABLAT?) AND L1
L3 732 S L1 AND PHOTODESOR?
L4 37 S L2-3 AND(IR OR INFRARED OR INFRA RED)
L5 242 S L2-3 AND(POLYACRYL? OR ACRYLAMID?)
L6 140 S (PHOTODESOR? OR LASER(2A)(DESOR? OR ABLAT?))/TI,IT,ST AND L5
L7 171 S L4,L6
L8 101 S L5 NOT L7
L9 1 S L8 AND MINIMALIST
L10 91 S L7 NOT PY>2000
L11 27 S L7 NOT L10 AND PATENT/DT
L12 33 S L7 NOT L10 AND 2001/PY
L13 47 S L11-12 NOT ELECTROBLOT?
L14 139 S L9-10,L13

=> d bib,ab 1-139

L14 ANSWER 17 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 136:163689 CA
TI System and method of **infrared** matrix-assisted **laser desorption**/ionization **mass spectrometry** in **polyacrylamide gels**
IN Haglung, Richard F., Jr.; Ermer, David R.; Baltz-Knorr, Michelle Lee
PA Vanderbilt University, USA
SO PCT Int. Appl., 53 pp.
PI WO 2002014849 A1 20020221 WO 2001-US25658 20010816
PRAI US 2000-225719P P 20000816
AB The invention concerns a system and method for desorption and ionization of analytes in an ablation medium. In one embodiment, the method includes the steps of prepg. a sample having analytes in a medium including at least one component, freezing the sample at a sufficiently low temp. so that at least part of the sample has a phase transition, and irradiating the frozen sample with short-pulse radiation to cause medium ablation and desorption and ionization of the analytes. The method further includes the steps of selecting a resonant vibrational mode of at least one component of the medium and selecting an energy source tuned to emit radiation substantially at the wavelength of the selected resonant vibrational mode. The medium is an **electrophoresis** medium having **polyacrylamide**. In one embodiment, the energy source is a laser, where the laser can be a free electron laser tunable to generate short-pulse radiation. Alternatively, the laser can be a solid state laser tunable to generate short-pulse radiation. The laser can emit light at various ranges of wavelength. Diagrams describing the app. assembly and operation are given.

L14 ANSWER 68 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 133:86282 CA
TI Interfacing matrix-assisted **laser desorption**/ionization **mass spectrometry** with column and planar separations
AU Gusev, A. I.
CS Research Laboratories, Rohm and Haas Company, Spring House, PA, 19477-0904, USA
SO Fresenius' Journal of Analytical Chemistry (2000), 366(6-7), 691-700
AB A review with 80 refs. This paper presents a crit. review of off-line and online coupling of matrix-assisted **laser desorption**/ ionization (MALDI) **mass spectrometry** to liq. column sepns. (e.g. HPLC, GPC and CE) and planar sepns.

(e.g. PAGE and TLC). Off-line MALDI anal. of fractions collected from HPLC, GPC and CE or spots scraped and extd. from TLC and PAGE has already become a routine practice for many labs. MALDI has also been used to obtain mass spectra directly from TLC plates and PAGE. The direct anal. methods range from dot-blotted samples to two-dimensional scanning of the entire **gels**/plates. Various combinations of online coupling of MALDI with column sepns. are also reviewed. The review discusses the strengths and limitations assocd. with different off-line and online coupling approaches.

L14 ANSWER 76 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 132:236378 CA
TI A method for characterization of humic and fulvic acids by **gel electrophoresis laser ablation** inductively coupled plasma **mass spectrometry**
AU Evans, R. Douglas; Villeneuve, Janice Y.
CS Environmental Sciences Centre, Trent University, Peterborough, ON, K9J 7B8, Can.
SO Journal of Analytical Atomic Spectrometry (2000), 15(2), 157-161
AB The coupling of **gel-electrophoresis** (GE) with **laser ablation** inductively coupled plasma **mass spectrometry** (LA-ICP-MS) has been used to measure the binding of lead to various mol. size fractions of humic and fulvic acids. Stable isotopic tracers were utilized to sep. the metals bound initially to the acids from those bound exptl. Ultimately, this technique will allow the detn. of the binding capacity of the acids for trace metals. Humic or fulvic acids were equilibrated with a stable isotopic metal tracer (206Pb). Sodium dodecyl sulfate **polyacrylamide gel electrophoresis** was used to sep. humic and fulvic acids as a function of size. **Gel** plates contg. the sepd. acids were dried and mounted on a microscope slide. **Laser ablation** was used to sample the plates at 50-100 mm intervals with the ablated material being analyzed by inductively coupled plasma **mass spectrometry**. Added metal and carbon concns. were measured simultaneously. The results can be used to det. variation in metal binding as a function of org. acid size and for fingerprinting org. acids from natural systems.

L14 ANSWER 80 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 132:163109 CA
TI Effect of experimental conditions on the analysis of sodium dodecyl sulphate **polyacrylamide gel electrophoresis** separated proteins by matrix-assisted **laser desorption**/ionisation **mass spectrometry**
AU Galvani, Marina; Bordini, Ellenia; Piubelli, Chiara; Hamdan, Mahmoud
CS Glaxo Wellcome Medicines Research Centre, Verona, 37135, Italy
SO Rapid Communications in Mass Spectrometry (2000), 14(1), 18-25
AB Two mixts. of proteins having mol. wts. in the range ~8-97 kDa were sepd. by SDS-PAGE (SDS-PAGE) and examd. by delayed extn. matrix-assisted **laser desorption**/ionization **mass spectrometry** (MALDI-MS). Part of our aim in this study is to gain more insight into the influence of the various exptl. conditions on the overall quality of the acquired mass spectral data. Different protein extn. procedures, two staining agents, and extn. times, were among the parameters assessed. In terms of the overall quality of the acquired mass spectra and the speed of protein recovery, ultrasonic assisted passive elution, into a solvent mixt. contg. formic acid/acetonitrile/2-isopropanol/water, was found to be more efficient than other elution procedures. The higher resoln. assocd. with the delayed extn. mode allowed the identification of a no. of protein modifications, including multiple formylation provoked by formic acid, cysteine alkylation caused by unpolymd. **acrylamide** monomers, and complexation with the staining reagents. The detection of these modifications, however, was limited to proteins under 30 kDa. Anal. of a ubiquitin tryptic digest by reflectron MALDI time-of-flight (TOF) allowed reliable identification of a no. of the formylation sites.

L14 ANSWER 81 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 132:134352 CA
TI Polyol ethers as matrices for matrix-assisted **laser desorption mass spectrometry** of biopolymers
IN Bruker, Daltonik Gmbh
PA Bruker Daltonik Gmbh, Germany
SO Ger. Offen., 10 pp.
PI DE 19834070 A1 20000210 DE 1998-19834070 19980729
GB 2340298 B2 20021204
PRAI DE 1998-19834070 A 19980729
AB The invention concerns the photoionization of biopolymers for matrix-assisted **laser desorption mass spectrometry** in a manner that does not produce fragments or adducts in order to det. the mol. wts. of the analyte by using polyol ethers with low b.p. and that are **IR** or UV adsorbents. The method is used for automated anal. of biopolymers. The matrix-forming polyol ethers are in aq. soln.; the matrix is applied into the hydrophilic compartments of a microtiterplate; the hydrophilic compartments are divided by hydrophobic rims. The analyte is a added directly or blotted in a previous process onto a membrane. Water from the matrix soln. is evapd. prior to placing the sample into the vacuum chamber. Erbium-YAG **IR**-lasers or UV emitting lasers are used; in the latter case, UV absorbents are added to the matrix.

L14 ANSWER 84 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 132:20761 CA
TI Ambient pressure matrix-assisted **laser desorption** ionization (MALDI) apparatus and method of analysis
IN Bai, Jian; Fischer, Steven M.; Flanagan, J. Michael
PA Hewlett-Packard Company, USA
SO Eur. Pat. Appl., 21 pp.
PI EP 964427 A2 19991215 EP 1999-111331 19990610
PRAI US 1998-89088P P 19980612
AB A **mass spectrometer** having a matrix-assisted **laser desorption** ionization (MALDI) source which operates at ambient pressure is disclosed. The app. and method are disclosed to analyze at least one sample which contains at least one analyte using MALDI. The app. includes: (a) an ionization enclosure including a passageway configured for delivery of ions to the mass anal. device; (b) means to maintain said ionization enclosure at an ambient pressure of greater than 13.3 Pa (100 mTorr); (c) a holder configured for maintaining a matrix contg. said sample in the ionization enclosure at said ambient pressure; (d) a source of laser energy including means assocd. with the ionization enclosure for directing the laser energy onto said matrix maintained by the holder at the ambient pressure to desorb and ionize at least a portion of the analyte in the sample, and (e) means for directing at least a portion of the at least one ionized analyte into the passageway. The ambient pressure (AP-MALDI) source is compatible with various mass analyzers, particularly with **mass spectrometers** and solves many problems assocd. with conventional MALDI sources operating under vacuum. Atm. pressure MALDI is described. The anal. of org. mols. or fragments thereof, particularly biomols., e.g., biopolymers and organisms, is described. An AP-MALDI **mass spectrometer** was prepd. and used to analyze a tryptic digest of bovine cytochrome c.

L14 ANSWER 90 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 131:155445 CA
TI Observation of sodium **gel**-induced protein modifications in dodecylsulfate **polyacrylamide gel electrophoresis** and its implications for accurate molecular weight determination of **gel**-separated proteins by matrix-assisted

laser desorption ionization time-of-flight **mass spectrometry**

AU Jeannot, Michael A.; Zheng, Jing; Li, Liang

CS Department of Chemistry, University of Alberta, Edmonton, AB, T6G 2G2, Can.

SO Journal of the American Society for Mass Spectrometry (1999), 10(6), 512-520

AB Matrix-assisted **laser desorption** ionization (MALDI) time-of-flight **mass spectrometry** (TOFMS) can potentially provide accurate mol. wt. information of proteins sepd. by sodium dodecylsulfate PAGE (SDS-PAGE). Several issues related to resoln. and accuracy of mol. wt. measurement are investigated by using a time-lag focusing MALDI-TOF **mass spectrometer**. The effects of the **gel** components SDS, glycerol, and Tris buffer on the mass spectral signals are studied systematically. Glycerol and tris buffer are shown to have little or no effect on resoln. and mass accuracy, whereas SDS degrades sensitivity, resoln., and mass accuracy even at low concns. A simple and fast **gel** extn. technique is presented which is capable of detecting proteins loaded at the low-picomole level on the **gel**. The sample prepn. procedure used in this work appears to remove most of SDS from the **gel**, thereby reducing the peak broadening effect caused by SDS and resulting in high resoln. and accurate measurement of proteins. However, for proteins contg. cysteines, the mol. ions are composed of a distribution of **acrylamide**-protein adducts likely formed by reaction with unpolymd. **acrylamide** in the **gel** during the **gel** sepn. process. The implications of **gel**-induced protein modifications on the accurate mol. wt. measurement of **gel**-sepd. proteins are discussed.

L14 ANSWER 103 OF 139 CA COPYRIGHT 2003 ACS on STN

AN 130:234195 CA

TI **Infrared** matrix-assisted **laser desorption**/ionization **mass spectrometry** with a transversely excited atmospheric pressure carbon dioxide laser at 10.6 μm wavelength with static and delayed ion extraction

AU Menzel, Christoph; Berkenkamp, Stefan; Hillenkamp, Franz

CS Institut fuir Medizinische Physik und Biophysik, Universitat Munster, Munster, D-48149, Germany

SO Rapid Communications in Mass Spectrometry (1999), 13(1), 26-32

AB **IR** matrix-assisted **laser desorption**/ionization **mass spectrometry** (**IR**-MALDI-MS) at 10.6 μm wavelength with static and delayed ion extn. is reported. A compact, sealed-off transversely excited atm. pressure carbon dioxide laser system with an output energy of 10 mJ per pulse and an initial spike of 70-90 ns duration was used for the expts. An Er:YAG laser (λ = 2.94 μm, t = 90 ns) in the **IR** and a frequency-tripled Nd:YAG laser (λ = 355 nm, t = 15 ns) in the UV were employed for comparison. A direct comparison of MALDI-MS in the reflectron mode of the **mass spectrometer** showed less metastable fragmentation for **IR**-MALDI with the CO2 laser as compared to UV-MALDI. As a result mass spectra of large biomols. up to several hundred kDa (KDa) in mass with a mass resoln. exceeding 100 (FWHM) were obtained in a reflectron time-of-flight **mass spectrometer**. A mass resoln. of up to 7000 (FWHM) and a mass accuracy of a few ppm for peptides is shown with delayed ion extn. Anal. sensitivity for CO2-MALDI-MS is in the low femtomole range. Mass spectra of **gel**-sepd. and electroblotted proteins desorbed directly from a PVDF membrane and of a double stranded DNA of 515 base pairs with the CO2 laser are shown as examples for applications.

L14 ANSWER 106 OF 139 CA COPYRIGHT 2003 ACS on STN

AN 129:158709 CA

TI Routine identification of proteins from sodium dodecyl sulfate-**polyacrylamide gel electrophoresis** (SDS-PAGE) **gels** or polyvinyl difluoride membranes using matrix assisted **laser desorption**/ionization-time of flight-**mass spectrometry** (MALDI-TOF-MS)

AU Fernandez, Joseph; Gharahdaghi, Farzin; Mische, Sheenah M.

CS DNA Technol. Center, Rockefeller Univ., New York, NY, 10021, USA
SO Electrophoresis (1998), 19(6), 1036-1045
AB As the resource lab. for Rockefeller University the author's emphasis continues to be on methodol. development for the routine anal. of low abundance proteins isolated from native sources. In the past 10 yr, **gel electrophoresis** of proteins has become the method of choice for the prepn. of microgram and submicrogram quantities of protein for primary structural characterization, and over 95% of the samples submitted for protein identification are either in a **gel** or bound to polyvinyl difluoride membranes (PVDF). The authors employ multiple microanal. approaches encompassing Edman sequence degrdn., amino acid and matrix assisted **laser desorption**/ionization-time of flight (MALDI-TOF) **mass spectrometric** anal. to provide an integrated protein characterization of such samples. The authors describe the 2 major services the authors employ when providing protein identification from in-**gel** or PVDF-bound proteins.

L14 ANSWER 107 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 129:92505 CA
TI **Gels** in vacuo? A **minimalist** approach for combining **mass spectrometry** and **polyacrylamide gel electrophoresis**
AU Loo, Rachel R. Ogorzalek; Andrews, Philip C.; Loo, Joseph A.
CS Department of Biological Chemistry, University of Michigan, Ann Arbor, MI, USA
SO Mass Spectrometry of Biological Materials (2nd Edition) (1998), 325-343. Editor(s): Larsen, Barbara S.; McEwen, Charles N. Publisher: Dekker, New York, N. Y.
AB This article describes methods that allow high-resoln. **gel electrophoresis** to be linked directly to the high throughput and sensitivity of matrix-assisted **laser desorption** ionization **mass spectrometry**.

L14 ANSWER 110 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 129:51118 CA
TI Additional possible tools for identification of proteins on one- or two-dimensional **electrophoresis**
AU Tsugita, Akira; Kamo, Masaharu; Miyazaki, Kenji; Takayama, Mitsuo; Kawakami, Takao; Shen, Ruqun; Nozawa, Takehiro
CS Research Inst. Biosciences, Science Univ. Tokyo, Noda, 278, Japan
SO Electrophoresis (1998), 19(6), 928-938
AB Addnl., essentially chem., identification methods of proteins in **polyacrylamide gel electrophoresis** are described. 2 Cleavages of peptide bonds were used at the C-side of aspartic acid with a 0.2% pentafluoropropionic acid (PFPA) aq. vapor at 90° for 4-16 h, and the N-side of Ser/Thr with an S-Et trifluorothioacetate vapor at 50° for 6-24 h. The products were analyzed by **mass spectrometry**-peptide mass fingerprinting. A new type of C-terminal sequencing at multisites of protein was introduced. An aq. vapor of 90% PFPA at 90° for 2-16 h provided cleavages at the C-side of aspartic acid and the N-side of Ser/Thr and simultaneous successive truncation at the C-termini of the cleaved fragments. The product resulted in C-terminal sequences at multisites in proteins by **mass spectrometric** anal. The following chem. deblocking methods were used. Anhyd. hydrazine vapor at -5° for 8 h deblocked the N-formyl group, and the vapor at 20° for 4 h deblocked pyrrolidone carboxylate. N-acetylSer/Thr was deblocked by aq. vapor of 75% PFPA at 50° for 1 h, followed by reaction with p-sulfophenylisothiocyanate at pH 6.0. These methods were applied to a variety of protein spots on **polyacrylamide gels**. A new stepwise C-terminal sequencing of protein from **polyacrylamide gels** is also described.

L14 ANSWER 116 OF 139 CA COPYRIGHT 2003 ACS on STN

AN 128:164683 CA
TI Development of methods for the charge-derivatization of peptides in **polyacrylamide gels** and membranes for their direct analysis using matrix-assisted **laser desorption**-ionization **mass spectrometry**
AU Strahler, John R.; Smelyanskiy, Yanina; Lavine, Gary; Allison, John
CS Dep. Biochem., Michigan State Univ., East Lansing, MI, 48824-1322, USA
SO International Journal of Mass Spectrometry and Ion Processes (1997), 169/170, 111-126
AB Approaches are being developed for the interfacing of matrix-assisted **laser desorption**-ionization (MALDI) **mass spectrometry** with PAGE, in which **laser**-irradiated samples **desorb** directly from a **gel**, or from a membrane on which **gel**-sepd. polypeptides have been transferred. Whether one- or two-dimensional **electrophoretic** sepns. have been performed, prepns. for the MALDI expt. which follow must optimize detection of the analytes present and the generation of structural information. Procedures have been developed for forming charged derivs. of peptides in soln. When subjected to MALDI anal., these charged derivs. produce ions in some cases where the underivatized peptide would not yield a response. The ions fragment following acceleration and yield informative and simple post-source decay (PSD) spectra. The development of approaches to interfacing this chem. with MALDI directly from **gels** and membranes is presented here.

L14 ANSWER 117 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 128:164643 CA
TI One step microelectroelution concentration method for efficient coupling of sodium dodecylsulfate **gel electrophoresis** and matrix-assisted **laser desorption** time-of-flight **mass spectrometry** for protein analysis
AU Clarke, Nigel J.; Li, Feng; Tomlinson, Andy J.; Naylor, Stephen
CS Biomedical Mass Spectrometry Facility, Mayo Clinic, Rochester, MN, USA
SO Journal of the American Society for Mass Spectrometry (1998), 9(1), 88-91
AB The coupling of the widely used sepn. technique of conventional sodium dodecylsulfate **polyacrylamide gel electrophoresis** (SDS-PAGE) with the mass accuracy measurement capability of **mass spectrometry** (MS) provides a very powerful anal. technique. However, at present, there is no simple, definitive method for coupling the two methods. Typically, sepd. proteins are extd. from the **gel**, either as the native protein or as a peptide mixt. after in-**gel** protolytic digestion, and then analyzed by **mass spectrometry**. However, the various extn. techniques described previously have been labor intensive and require a large no. of steps. The **mass spectrometry** anal. of very low concns. of in vivo derived proteins requires min. sample handling and online concn. Therefore, we have developed an efficient microelectroelution technique that is applied in a single step manner and contains an online concn. device. Initial results from this system have shown a high efficiency of analyte elution from the **gel** and a simple, robust technique for the coupling of SDS-contg. **gels** with MALDI-TOF-MS anal. and a capability of analyzing proteins at the subpicomole level.

L14 ANSWER 119 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 128:32076 CA
TI **Polyacrylamide Gel Electrophoresis** Coupled with Matrix-Assisted **Laser Desorption**/Ionization **Mass Spectrometry** for tRNA Mutant Analysis
AU Wei, Jing; Lee, Cheng S.
CS Department of Chemistry and Ames Laboratory USDOE, Iowa State University, Ames, IA, 50011, USA
SO Analytical Chemistry (1997), 69(23), 4899-4904
AB In analogy to two-dimensional anal., the mobility shift in native **polyacrylamide gel electrophoresis** (PAGE) due to a nucleotide substitution of a single-stranded tRNA (tRNA) fragment serves as the first dimension for

tRNA mutation anal. Matrix-assisted **laser desorption**/ionization **mass spectrometry** (MALDI-MS), as the second dimension, allows precise detn. of the mass of the tRNA fragments resolved by native PAGE. Off-line combination of native PAGE with MALDI-MS is demonstrated for high-resoln. anal. of tRNAval and its mutants, including a three-nucleotide deletion and 12 single-base substitutions. Three approaches, including direct extn. of tRNAs from **gel** into buffer soln., dissoln. of membrane in the matrix soln., and direct desorption of tRNAs from the membrane, are studied for coupling native PAGE with MALDI-MS. The membrane dissoln. method is simple, and the resulting mixt. is amenable to MALDI-MS anal. In the membrane dissoln. method, as little as 1 μg or 40 pmol of tRNA sample is loaded on a native **gel**, sepd., capillary eluted onto a nitrocellulose membrane, and recovered using the matrix soln. of 2,4,6-trihydroxyacetophenone in acetone.

L14 ANSWER 120 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 128:32037 CA
TI Identification of the Components of Simple Protein Mixtures by High-Accuracy Peptide Mass Mapping and Database Searching
AU Jensen, Ole N.; Podtelejnikov, Alexandre V.; Mann, Matthias
CS Protein Peptide Group, European Molecular Biology Laboratory (EMBL), Heidelberg, D-69117, Germany
SO Analytical Chemistry (1997), 69(23), 4741-4750
AB Peptide mass mapping by matrix-assisted **laser desorption**/ionization (MALDI) followed by database searching with the set of measured peptide masses is now a powerful method for the identification of pure proteins. Protein mixts.-such as frequently occur due to comigration in **polyacrylamide gel** bands-have hitherto required protein sequencing. Here we demonstrate that such protein bands can also be analyzed by peptide mass mapping alone. Database searching with the complete list of peptide masses detd. by delayed-extn. MALDI **mass spectrometry** with a mass error of less than 30 ppm retrieves the most prominent protein in a mixt. In a second step, the protein identity is further confirmed by matching as many of the measured peptide masses as possible to the retrieved amino acid sequence. Peptide masses remaining after this "pass search" are searched again to identify the next component in the protein mixt. This iterative process is repeated until all major ion signals are accounted for. Protein mixts. consisting of two or more individual components in a single **gel** band can be analyzed, further increasing the general applicability of MALDI peptide mapping for protein identification.

L14 ANSWER 124 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 127:106175 CA
TI Analysis of Proteins by Direct-Scanning **Infrared**/MALDI **Mass Spectrometry** after 2D-PAGE Separation and Electroblotting
AU Eckerskorn, Christoph; Strupat, Kerstin; Schleuder, Detlev; Hochstrasser, Denis; Sanchez, Jean-Charles; Lottspeich, Friedrich; Hillenkamp, Franz
CS Institute for Medical Physics and Biophysics, University of Muenster, Muenster, D-48149, Germany
SO Analytical Chemistry (1997), 69(15), 2888-2892
AB A novel approach is reported for the anal. and identification of proteins sepd. by 2D-PAGE with scanning **IR** matrix-assisted **laser desorption**/ionization **mass spectrometry** (scanning **IR**/MALDI-MS). The proteins of human blood plasma were sepd. by 2D-PAGE, electroblotted onto PVDF membranes, incubated in matrix soln., and then scanned by **IR**/MALDI-MS. Mass contour plots of selected spots were obtained. Protein sepn. is shown to be conserved by comparison with silver-stained **gels**. The sensitivity for the protein detection is comparable if not better than that of silver-stained **gels**. Post-translational modifications were identified by comparing the

measured mass to the one calcd. from the known DNA sequence. Adduct formation to unprotected cysteine residues during **gel** sepn. is demonstrated for selected proteins.

L14 ANSWER 125 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 127:92314 CA
TI Sensitivity and mass accuracy for proteins analyzed directly from **polyacrylamide gels**: implications for proteome mapping
AU Loo, Rachel R. Ogorzalek; Mitchell, Charles; Stevenson, Tracy I.; Martin, Stephen A.; Hines, Wade M.; Juhasz, Peter; Patterson, Dale H.; Peltier, John M.; Loo, Joseph A.; Andrews, Philip C.
CS Department Biological Chemistry, University Michigan, Ann Arbor, MI, USA
SO Electrophoresis (1997), 18(3-4), 382-390
AB Matrix-assisted **laser desorption** ionization (MALDI) mass spectra were obtained directly from thin-layer isoelec. focusing (IEF) **gels** with as little as 700 fmol of α- and β-chain bovine Hb and bovine carbonic anhydrase, and 2 pmol of bovine trypsinogen, soybean trypsin inhibitor, and bovine serum albumin all loaded onto a single lane. By soaking the **gel** in a matrix soln., matrix was deposited over the entire **gel** surface, allowing MALDI scanning down complete lanes of the one-dimensional **gel**. As long as matrix crystals were deposited finely on the surface of the **gel**, time-lag focusing techniques were capable of ameliorating some of the mass accuracy limitations inherent in desorbing from uneven insulator surfaces with external calibration. Eleven measurements on the 5 kDa α-subunit proteins of lentil lectin measured over the course of 1 h and referenced to a single calibration yielded a std. deviation of 0.025%. Colloidal gold staining was compatible with desorption directly from IEF and SDS-**polyacrylamide gels**. This direct approach simplifies the interface between **gel electrophoresis** and **mass spectrometry** dramatically, making the process more amenable to automation.

L14 ANSWER 128 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 125:269749 CA
TI Interfacing **polyacrylamide gel electrophoresis** with **mass spectrometry**
AU Loo, R. R. Ogorzalek; Mitchell, C.; Stevenson, T.; Loo, J. A.; Andrews, P. C.
CS Dept. Biological Chemistry, University Michigan, Ann Arbor, MI, 48109-0674, USA
SO Techniques in Protein Chemistry VII, [Symposium of the Protein Society], 9th, Boston, July 8-12, 1995 (1996), Meeting Date 1995, 305-313. Editor(s): Marshak, Daniel R. Publisher: Academic, San Diego, Calif.
AB A method is described for acquiring mass spectra directly from **electrophoretic gels**, without electroelution or electroblotting. The method relies upon ultrathin **polyacrylamide gels** that dry to thicknesses of ≤10 μ and that have the addnl. advantages of rapid prepn. and run times. Spectra were acquired from isoelec. focusing, native, and SDS **gels**. It is also possible to run virtual 2-dimensional **gels** in which proteins are resolved in the 1st dimension on the basis of their charge while the 2nd-dimension is matrix-assisted **laser-desorption** ionization **mass spectrometry** instead of SDS **gel electrophoresis**. A simple mixt. of proteins is analyzed by this approach. A 2nd method, diffusive transfer, is shown to overcome many of the problems assocd. with electroblotting to membranes. The authors examine the products of CNBr digestion in-**gel** and demonstrate its utility for peptide mapping applications.

L14 ANSWER 134 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 124:337236 CA
TI **Infrared**-matrix-assisted **laser desorption**/ionization **mass spectrometry** (IR-

MALDI-MS) of proteins electroblotted onto polymer membranes after SDS-PAGE separation
AU Strupat, Kerstin; Eckerskorn, Christoph; Karas, Michael; Hillenkamp, Franz
CS Institute Medical Physics and Biophysics, University Munster, Muenster, 48149, Germany
SO Mass Spectrometry in the Biological Sciences (1996), 203-16. Editor(s): Burlingame, A. L.; Carr, Steven A. Publisher: Humana, Totowa, N. J.
AB The feasibility of using matrix-assisted **laser desorption mass spectrometry** (MALDI-MS) for anal. of proteins electroblotted onto polymer substrates after a one dimensional SDS-PAGE (1D-SDS-PAGE) sepn. of a protein mixt. has been reported recently. In this paper, the current state-of-the-art is summarized and exemplified by focusing on some fundamental anal. aspects, such as the mass range accessible, the application to hydrophilic membranes, the sample consumption per laser shot, the compatibility with different matrixes and different staining materials as well as the accuracy of mass detn.

L14 ANSWER 136 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 122:182699 CA
TI Thin-layer chromatography/**laser desorption** of peptides followed by multiphoton ionization time-of-flight **mass spectrometry**
AU Krutchinsky, A. N.; Dolgin, A. I.; Utsal, O. G.; Khodorkovski, A. M.
CS Lepta-Petersburg Ltd., Dobrolubova, Petersburg, 197198, Russia
SO Journal of Mass Spectrometry (1995), 30(2), 375-9
AB The location of the sepd. compds. of GlnTrp/GlyTyr and pentagastrin/gramicidin D peptide model mixts. on silica **gel** and cellulose thin-layer chromatog. plates has been examd. by **laser desorption** multiphoton ionization time-of-flight **mass spectrometry**. The multiphoton ionization mass spectra of neutrals desorbed by sequential scanning of the thin-layer chromatog. plates vs. the **IR** laser spot allowed imaging of the distribution profile of the compds. The method appeared to be promising for the anal. of thin-layer chromatograms.

L14 ANSWER 137 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 120:318607 CA
TI Identification of proteins in **polyacrylamide gels** by **mass spectrometric** peptide mapping combined with database search
AU Mortz, Ejvind; Vorm, Ole; Mann, Matthias; Roepstorff, Peter
CS Dep. Mol. Biol., Odense Univ., Odense, 5230, Den.
SO Biological Mass Spectrometry (1994), 23(5), 249-61
AB **Mass spectrometric** peptide mapping of proteins sepd. by one-dimensional SDS-PAGE has been investigated. The best results are obtained after blotting of the proteins onto polyvinylidene difluoride membranes followed by enzymic digestion of the protein on the membrane. The peptide maps were investigated in terms of completeness and applicability for protein identification using a previously developed database search program as well as for the possibility for full characterization of covalent modifications in the proteins. The most complete peptide maps were obtained when the proteins were reduced and alkylated on the membrane prior to enzymic digestion followed by sepn. of the resulting mixt. by HPLC prior to **mass spectrometric** anal. Such peptide maps cover up to 98% of the sequence and consequently may allow complete characterization of post-translational modifications in proteins for which the amino acid sequence is known. The fastest and most sensitive procedure to obtain peptide maps sufficient for protein identification was direct anal. of the extd. peptide mixt. by matrix-assisted **laser desorption** ionization (MALDI) **mass spectrometry**. The use of external and internal calibration of MALDI spectra for database searches is evaluated as well as the possibility of including a post-calibration routine

within the search program.

L14 ANSWER 138 OF 139 CA COPYRIGHT 2003 ACS on STN
AN 120:100945 CA
TI Matrix-assisted **laser desorption** ionization **mass spectrometry** of proteins electroblotted after **polyacrylamide gel electrophoresis**
AU Strupat, Kerstin; Karas, Michael; Hillenkamp, Franz; Eckerskorn, Christoph; Lottspeich, Friedrich
CS Inst. Med. Phys. Biophys., Univ. Muenster, Muenster, 48149, Germany
SO Analytical Chemistry (1994), 66(4), 464-70
AB Matrix-assisted **laser desorption** ionization **mass spectrometry** (Maldi-MS) of proteins, electroblotted onto polymer membranes after SDS-PAGE sepn. is demonstrated. The proteins are desorbed directly from the blot membranes after matrix application. Desorption with 2.94-μm **IR** radiation and succinic acid as matrix was found superior to 355-nm UV desorption using 2,5-dihydroxybenzoic acid as matrix. Several com. available membranes tested resulted in protein signals after matrix incubation of the membrane. Systematic investigations for five different poly(vinylidene fluoride) (PVDF) membranes showed improved results for membranes exhibiting high sp. surfaces. The matrix should be applied immediately after the blotting procedure while the blot is still wet. Lateral resoln. of the protein band is preserved after the MALDI prepn. procedure. Staining with org. dyes results in broad protein signals shifted in mass due to addn. of several dye mols.; staining with colloidal stains such as colloidal gold or India ink somewhat deteriorates the quality of the spectra, but renders the correct protein mass.

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